

```

Query Match      100.0%;      Score 20;      DB 16;      Length 1436;
Best Local Similarity 100.0%;      Pred. NO. 1.06e-01;
Matches 20;      Conservative      0;      Mismatches 0;      Indels 0;      Gaps 0;

```

b	841	CAGCTTGCTCTGCGTCGACG	860
y	1	cagcttgctcttcgctgcacg	20

For SEQIDNO 1

RESULT	2	SS16SRDNG	1459 bp	DNA
LOCUS		S.shomron	16S rRNA gene.	
DEFINITION		X80678		
ACCSSION		G1240062		
ID		16S ribosomal RNA.		
KEYWORDS		Salmonella shomron.		
SOURCE		Salmonella shomron		
ORGANISM		Eubacteria; Proteobacteria;	gamma subdivision;	Enterobacteriaceae;
		Salmonella.		

29-MAR-1996 BCT

REFERENCE
AUTHORS
TITLE
1 (bases 1 to 1459)
Cilia,V., Lafay,B. and Christen,R.
Existence of sequence heterogeneities among the seven operons of
the rrr family in *Escherichia coli* - Small subunit ribosomal RNA
heterogeneity, phylogenetic and taxonomic implications
Unpublished
2 (bases 1 to 1459)
Lafay,B.
Direct Submission
Submitted (26-JUL-1994) B. Lafay, CNRS & Universite Paris 6,
Station Zoologique, Observatoire Oceanologique, Villefranche Sur
Mer, 06230, FRANCE
3 (bases 1 to 1459)
Cilia,V., Lafay,B. and Christen,R.
Sequence heterogeneities among 16S ribosomal RNA sequences, and
their effect on phylogenetic analyses at the species level
Mol Biol Evol 13 (3): 451-461 (1996)

```

JOURNAL      MOI: Biol. Evol. 25 (1977)
MEDLINE      96351315
FEATURES
  source      Location/Qualifiers
              1. .1459
              /organism="salmonella shomron"
              /db_xref="taxon:46627"
              1. .1459
              /product="16S ribosomal RNA"
BASE COUNT   368 a 332 c 463 g 282 t 14 others
ORIGIN
Query Match   100.0%; Score 20; DB 16; Length 1459;
Best Local Similarity 100.0%; Pred. No. 1.06e-01;
Matches       20; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

	BCT	21-MAR-1997
Dd	80 CAGCTTGCTTCGCTGCAC	99
Qy	1 cagcttgccttcgctcac	20
RESULT	3	
LOCUS	STU90316	1541 bp DNA
DEFINITION	Salmonella typhimurium StmI 16S ribosomal RNA gene, complete sequence.	
ACCSSION	U90316	
NID	g1899235	
KEYWORDS	Salmonella typhimurium.	
SOURCE	Salmonella typhimurium	
ORGANISM	Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae	
	1 (bases 1 to 1541)	
	Germaniaum,G. and Pang,T.	
	Institute for Advanced Studies, Universiti 50603, West Malaysia	

```

/organism="Salmonella typhimurium"
/strain="Stm1"
/db_xref="taxon:602"
1. 1541
/product="16S ribosomal RNA"
387 a 356 c 486 g 312 t
rRNA
BASE COUNT
ORIGIN

```

```

Query Match      100.0%; Score 20; DB 16; Length 1541;
Best Local Similarity 100.0%; Pred. No. 1.06e-01;
Matches          20; Conservative 0; Mismatches 0; Indels

```

Db	80	CAGCTTGCTCTTCGTGACG	99
Qy	1	cagcttgctattcgctgacg	20

RESULT	4				BCT	21-MAR-1997
LOCUS		SEP90318	1541 bp	DNA		
DEFINITION		Salmonella enteritidis SE22	16S ribosomal RNA gene, complete sequence.			
ACCESSION		U90318				
NID		g1899237				
KEYWORDS						
SOURCE		Salmonella enteritidis.				
ORGANISM		Salmonella enteritidis				
		Eubacteria; Proteobacteria;	gamma subdivision; Enterobacteriaceae;			
		Salmonella.				
REFERENCE		1. (bases 1 to 1541)				
AUTHORS		Subramaniam,G. and Pang,T.				
TITLE		Direct Submission				
JOURNAL		Submitted (21-FEB-1997)	Institute for Advanced Studies, University			
		of Malaya, Kuala Lumpur 50603,	West Malaysia			
		Location/Qualifiers				

```

FEATURES
    source
    1. 1541
    /organism="Salmonella enteritidis"
    /strain="SE22"
    /db_xref="taxon:592"
    1. 1541
    /product="16S ribosomal RNA"
    1480.0 314 t

```

BASE COUNT	390 a	357 c	480 y	321 c
ORIGIN				
Query Match		100.0%;	Score 20;	DB 16; Length 1541;
Best Local Similarity		100.0%;	Pred. No. 1.06e-01;	
Matches	20; Conservative	0;	Mismatches	0; Indels

db 80 CAGCTTGCTCTTCGCTGACG 99
 |||||
qy 1 cagcttgccttcgctgacg 20

5	ECOPROT	4248 bp	DNA	BCT.	03-MAR-1994
RESULT					
LOCUS					
DEFINITION	E. coli ATP-dependent protease binding subunit (clpB) gene, complete				
	3,333-3,465 bp, 1,132 aa, 165 CDS, 5' end.				

ACCESSION M29364 J01699 V00350
NID g147363
KEYWORDS 16S ribosomal RNA; ATP-binding protein; ATP-dependent protease; ATP-protease.
SOURCE E.coli (strain K-12), clone pLC[23,30].
ORGANISM Escherichia coli [bacteria, gamma subdivision: Enterobacteriaceae]

Eubacteria; Proteobacteria; gamma subphylum.
Escherichia.
1 (bases 2813 to 3930)
Shen W.-F., Squires, C.L. and Squires, C.L.
Nucleotide sequence of the rrrG ribosomal RNA promoter region of
Escherichia coli
Nucleic Acids Res. 10, 3303-3313 (1982)
8247208
2 (bases 1 to 3130)
Squires, C.L., Pedersen, S., Ross, B.M. and Squires, C.L.
CipB is the Escherichia coli heat shock protein F94.1
JOURNAL MEDLINE
REFERENCE
AUTHORS
TITLE

Phylogenetic analysis and identification of *Shigella* spp. by molecular probes

JOURNAL Mol. Cell. Probes 11 (6), 427-432 (1997)

MEDLINE 98164113

REFERENCE 2 (bases 1 to 1487)

AUTHORS Wang, R.

TITLE Direct Submission

JOURNAL Submitted (28-MAR-1996) R. Wang, Microbiology Division, National Center for Toxicological Research, FDA, 3900 NCTR DR., Jefferson, AR 72079, USA

FEATURES

source Location/Qualifiers

1..1487

/organism="Shigella dysenteriae"

/note="ATCC 13313"

/db_xref="taxon:622"

1..1487

/gene="16S rRNA"

/product="16S ribosomal RNA"

1..1487

/gene="16S rRNA"

BASE COUNT 375 a 341 c 472 g 299 t

ORIGIN

Query Match 90.0%; Score 18; DB 16; Length 1487;

Best Local Similarity 95.0%; Pred. No. 3.85e+00;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 57 AAGAGCTTGTCTTGTCT 76

|||||

QY 1 aaagcagctgtcttcttgc 20

RESULT 7

LOCUS A14556 31 bp DNA PAT 29-SEP-1994

DEFINITION Hybridization probe number 9 for the detection of *Escherichia coli*.

ACCESSION A14556

NID 9640877

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 31)

AUTHORS Rossau, R. and Van Heuverswijn, H.

TITLE Hybridization probes for detecting neisseria strains

JOURNAL Patent: EP 0337896-A 87 18-OCT-1989;

N.V. INNOGENETICS S.A.

FEATURES

source Location/Qualifiers

1..31

/organism="Artificial sequences"

BASE COUNT 8 a 6 c 9 g 8 t

ORIGIN

Query Match 85.0%; Score 17; DB 22; Length 31;

Best Local Similarity 94.7%; Pred. No. 1.53e+01;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 9 AAGAGCTTGTCTTGTCT 27

|||||

QY 2 aagcagctgtcttcttgc 20

RESULT 8

LOCUS A37179 185 bp DNA PAT 05-MAR-1997

DEFINITION Sequence 52 from Patent WO9403634.

ACCESSION A37179

NID 92294344

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 185)

AUTHORS Grau, O., Kovacic, R. and Griffiths, R.

TITLE OLIGONUCLEOTIDE SEQUENCES FOR THE SPECIFIC DETECTION OF MOLLICUTES

BY AMPLIFICATION OF PRESERVED GENES

Patent: WO 9403634-A 52 17-FEB-1994;

PASTEUR INSTITUT (FR)

Other publication FR 2694768 940218.

COMMENT Location/Qualifiers

source

1..185

/organism="unidentified"

/db_xref="taxon:32844"

BASE COUNT 50 a 40 c 59 g 36 t

ORIGIN

Query Match 85.0%; Score 17; DB 22; Length 185;

Best Local Similarity 94.7%; Pred. No. 1.53e+01;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 29 AAGAGCTTGTCTTGTCT 47

|||||

QY 2 aagcagctgtcttcttgc 20

RESULT 9

LOCUS ECRNG 1436 bp DNA BCT 07-JUL-1995

DEFINITION Start of the *E. coli* gene for 16S rRNA. Also contains part of unknown reading frame.

ACCESSION V00350

NID 942885

KEYWORDS 16S ribosomal RNA; ribosomal RNA; unidentified reading frame.

SOURCE *Escherichia coli*.

ORGANISM *Escherichia coli*.

REFERENCE 1 (bases 1 to 1436)

AUTHORS Shen, W.F., Squires, C. and Squires, C.L.

TITLE Nucleotide sequence of the rrrG ribosomal RNA promoter region of *Escherichia coli*

JOURNAL Nucleic Acids Res. 10 (10), 3303-3313 (1982)

MEDLINE 82247208

FEATURES

source Location/Qualifiers

1..1436

/organism="Escherichia coli"

/db_xref="taxon:562"

<1..345

/note="messenger RNA (3' end not sure)"

CDS

<1..318

/note="unknown reading frame"

/codon_start=1

/transl_table=11

/db_xref="PID:942886"

/db_xref="SWISS-PROT:P03815"

/translation="FINRIDEVYVHPLGEOHTASTAQIOLKRLYKRLERGVYEHIS

DEALKLISENGYDPVYGARPLKRAIOOQIENPLAQIILSGELVPGKVRILEVNEDRIV

AVQ"

762..>1436

/note="16S rRNA"

BASE COUNT 393 a 316 c 404 g 323 t

ORIGIN

Query Match 85.0%; Score 17; DB 16; Length 1436;

Best Local Similarity 94.7%; Pred. No. 1.53e+01;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 838 AAGAGCTTGTCTTGTCT 856

|||||

QY 2 aagcagctgtcttcttgc 20

RESULT 10

LOCUS SS16SRDNG 1459 bp DNA BCT 29-MAR-1996

DEFINITION S. shomron 16S rRNA gene.

ACCESSION X80678

NID g1240062

KEYWORDS 16S ribosomal RNA.

SOURCE *Salmonella shomron*.

FOR 94 ID NO 2

ORGANISM Salmonella shomron
Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.
REFERENCE 1 (bases 1 to 1459)
AUTHORS Cilia, V., Lafay, B. and Christen, R.
TITLE Existence of sequence heterogeneities among the seven operons of the rrr family in Escherichia coli - Small subunit ribosomal RNA heterogeneity, phylogenetic and taxonomic implications
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1459)
AUTHORS Lafay, B.
TITLE Direct Submission
JOURNAL Submitted (26-JUL-1994) B. Lafay, CNRS & Universite Paris 6, Station Zoologique, Observatoire Oceanologique, Villefranche Sur Mer, 06230, FRANCE
REFERENCE 3 (bases 1 to 1459)
AUTHORS Cilia, V., Lafay, B. and Christen, R.
TITLE Sequence heterogeneities among 16S ribosomal RNA sequences, and their effect on phylogenetic analyses at the species level
JOURNAL Mol. Biol. Evol. 13 (3), 451-461 (1996)
MEDLINE 96351315
FEATURES
source Location/Qualifiers
1..1459
/organism="Salmonella shomron"
/db_xref="taxon:46627"
rRNA 1..1459
/product="16S ribosomal RNA"
BASE COUNT 368 a 332 c 463 g 282 t 14 others
ORIGIN

Query Match 85.0%; Score 17; DB 16; Length 1459;
Best Local Similarity 94.7%; Pred. No. 1.53e+01;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 77 AAGCAGCTTGCTCTTCGCT 95
|||||
QY 2 aagcagcttgctcttgc 20

RESULT 11
LOCUS SEU90318 1541 bp DNA BCT 21-MAR-1997
DEFINITION Salmonella enteritidis SE22 16S ribosomal RNA gene, complete sequence.
ACCESSION U90318
NID g1899237
KEYWORDS Salmonella enteritidis.
SOURCE Salmonella enteritidis.
ORGANISM Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Salmonella.
REFERENCE 1 (bases 1 to 1541)
AUTHORS Subramaniam, G. and Pang, T.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-1997) Institute for Advanced Studies, University of Malaya, Kuala Lumpur 50603, West Malaysia
FEATURES
source Location/Qualifiers
1..1541
/organism="Salmonella enteritidis"
/strain="SE22"
rRNA 1..1541
/db_xref="taxon:592"
BASE COUNT 390 a 357 c 480 g 314 t
ORIGIN
Query Match 85.0%; Score 17; DB 16; Length 1541;
Best Local Similarity 94.7%; Pred. No. 1.53e+01;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 77 AAGCAGCTTGCTCTTCGCT 95
|||||
QY 2 aagcagcttgctcttgc 20

RESULT 12
LOCUS SBV90314 1541 bp DNA BCT 21-MAR-1997
DEFINITION Salmonella blockley Sbl 16S ribosomal RNA gene, complete sequence.
ACCESSION U90314
NID g1899233
KEYWORDS Salmonella blockley.
SOURCE Salmonella blockley.
ORGANISM Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Salmonella.
REFERENCE 1 (bases 1 to 1541)
AUTHORS Subramaniam, G. and Pang, T.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-1997) Institute for Advanced Studies, University of Malaya, Kuala Lumpur 50603, West Malaysia
FEATURES
source Location/Qualifiers
1..1541
/organism="Salmonella blockley"
/strain="Sbl"
/db_xref="taxon:57741"
rRNA 1..1541
/product="16S ribosomal RNA"
BASE COUNT 389 a 352 c 488 g 312 t
ORIGIN
Query Match 85.0%; Score 17; DB 16; Length 1541;
Best Local Similarity 94.7%; Pred. No. 1.53e+01;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 77 AAGCAGCTTGCTCTTCCT 95
|||||
QY 2 aagcagcttgctcttgc 20

RESULT 13
LOCUS SCU92192 1541 bp DNA BCT 01-APR-1997
DEFINITION Salmonella chingola 16S ribosomal RNA gene, complete sequence.
ACCESSION U92192
NID g1916304
KEYWORDS Salmonella chingola.
SOURCE Salmonella chingola.
ORGANISM Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Salmonella.
REFERENCE 1 (bases 1 to 1541)
AUTHORS Subramaniam, G. and Pang, T.
TITLE Direct Submission
JOURNAL Submitted (28-FEB-1997) Institute for Advanced Studies, University of Malaya, Kuala Lumpur 50603, Malaysia
FEATURES
source Location/Qualifiers
1..1541
/organism="Salmonella chingola"
/strain="Schl"
rRNA 1..1541
/db_xref="taxon:58099"
BASE COUNT 387 a 353 c 491 g 310 t
ORIGIN
Query Match 85.0%; Score 17; DB 16; Length 1541;
Best Local Similarity 94.7%; Pred. No. 1.53e+01;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 77 AAGCAGCTTGCTCTTCCT 95
|||||
QY 2 aagcagcttgctcttgc 20

RESULT 14
LOCUS A14565 1541 bp DNA PAT 29-SEP-1994
DEFINITION 16S rRNA.
ACCESSION A14565

Cilia, V., Lafay, B. and Christen, R.
 Sequence heterogeneities among 16S ribosomal RNA sequences, and
 their effect on phylogenetic analyses at the species level
 Mol. Biol. Evol. 13 (3), 451-461 (1996)
 JOURNAL 96351315
 REFERENCE 2 (bases 1 to 1385)
 AUTHORS Lafay, B.
 TITLE Direct Submission
 JOURNAL Submitted (26-JUL-1994) B. Lafay, CNRS & Universite Paris 6,
 Station Zoologique, Observatoire Oceanologique, Villefranche Sur
 Mer, 06230, FRANCE
 FEATURES Location/Qualifiers
 source 1. .1385
 /organism="Escherichia coli"
 /strain="PK3"
 /db_xref="taxon:562"
 1. .1385
 /gene="rrnE"
 /product="16S ribosomal RNA"
 1. .1385
 /gene="rrnE"
 347 a 318 c 440 g 273 t 7 others
 BASE COUNT
 ORIGIN
 Query Match 100.0%; Score 21; DB 16; Length 1385;
 Best Local Similarity 100.0%; Pred. No. 1.54e-01;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 38 GAAGCTTGCTTCTTGTGAC 58
 |||||
 1 gaagcttgcttcttctgac 21
 QY 1 gaagcttgcttcttctgac 21
 RESULT 6 ECRNHPK3 1417 bp DNA BCT 29-MAR-1996
 LOCUS E. coli rrnH gene.
 DEFINITION X80730
 ACCESSION g1240031
 NID 16S ribosomal RNA; 16S rRNA gene; 16S small subunit ribosomal RNA.
 KEYWORDS Escherichia coli.
 SOURCE Escherichia coli.
 ORGANISM Escherichia.
 REFERENCE 1 (bases 1 to 1417)
 AUTHORS Cilia, V., Lafay, B. and Christen, R.
 TITLE Sequence heterogeneities among 16S ribosomal RNA sequences, and
 their effect on phylogenetic analyses at the species level
 JOURNAL Mol. Biol. Evol. 13 (3), 451-461 (1996)
 MEDLINE 96351315
 REFERENCE 2 (bases 1 to 1417)
 AUTHORS Lafay, B.
 TITLE Direct Submission
 JOURNAL Submitted (26-JUL-1994) B. Lafay, CNRS & Universite Paris 6,
 Station Zoologique, Observatoire Oceanologique, Villefranche Sur
 Mer, 06230, FRANCE
 FEATURES Location/Qualifiers
 source 1. .1417
 /organism="Escherichia coli"
 /strain="PK3"
 /db_xref="taxon:562"
 1. .1417
 /gene="rrnH"
 /product="16S ribosomal RNA"
 1. .1417
 /gene="rrnH"
 357 a 325 c 450 g 280 t 5 others
 BASE COUNT
 ORIGIN
 Query Match 100.0%; Score 21; DB 16; Length 1417;
 Best Local Similarity 100.0%; Pred. No. 1.54e-01;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 37 GAAGCTTGCTTCTTGTGAC 57

|||||
 QY 1 gaagcttgcttcttctgac 21
 RESULT 7 PSU85856 1428 bp DNA BCT 20-AUG-1997
 LOCUS Pseudoalteromonas sp. IC006 16S ribosomal RNA gene, partial
 DEFINITION sequence.
 ACCESSION U85856
 NID g1850388
 KEYWORDS Pseudoalteromonas sp.
 SOURCE Pseudoalteromonas sp.
 ORGANISM Eubacteria; Proteobacteria; gamma subdivision; Pseudoalteromonas.
 REFERENCE 1 (bases 1 to 1428)
 AUTHORS Bowman, J.P., McCammon, S.A., Brown, M.V., Nichols, D.S. and
 McMeekin, T.A.
 TITLE Diversity and association of psychrophilic bacteria in Antarctic
 sea ice
 JOURNAL Appl. Environ. Microbiol. 63 (8), 3068-3078 (1997)
 MEDLINE 97394931
 REFERENCE 2 (bases 1 to 1428)
 AUTHORS Bowman, J.P., McCammon, S.A., Brown, M.V. and McMeekin, T.A.
 TITLE Direct Submission
 JOURNAL Submitted (21-JAN-1997) Antarctic CRC, University of Tasmania, GPO
 Box 252-80, Hobart, Tasmania 7001, Australia
 FEATURES Location/Qualifiers
 source 1. .1428
 /organism="Pseudoalteromonas sp."
 /strain="IC006"
 /db_xref="taxon:53249"
 <1. .>1428
 /product="16S ribosomal RNA"
 365 a 324 c 441 g 298 t
 BASE COUNT
 ORIGIN
 Query Match 100.0%; Score 21; DB 16; Length 1428;
 Best Local Similarity 100.0%; Pred. No. 1.54e-01;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 53 GAAGCTTGCTTCTTGTGAC 73
 |||||
 QY 1 gaagcttgcttcttctgac 21
 RESULT 8 HVU15102 1439 bp DNA BCT 16-MAR-1995
 LOCUS Hydrothermal vent eubacterium PVB_OTU_2 clone PVB_63, small subunit
 DEFINITION rRNA gene.
 ACCESSION U15102
 NID g710311
 KEYWORDS hydrothermal vent eubacterium PVB_OTU_2.
 SOURCE hydrothermal vent eubacterium PVB_OTU_2
 ORGANISM Eubacteria.
 REFERENCE 1 (bases 1 to 1439)
 AUTHORS Moyer, C.L., Dobbs, F.C. and Karl, D.M.
 TITLE Phylogenetic diversity of the bacterial community from a microbial
 mat at an active, hydrothermal vent system, Hawaii
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1439)
 AUTHORS Moyer, C.L.
 TITLE Direct Submission
 JOURNAL Submitted (26-SEP-1994) Craig L. Moyer, Department of Oceanography,
 University of Hawaii, 1000 Pope Road, Honolulu, HI 96822, USA
 FEATURES Location/Qualifiers
 source 1. .1439
 /organism="hydrothermal vent eubacterium PVB_OTU_2"
 /db_xref="taxon:37373"
 /clone="PVB_63"
 /clone_lib="Pele's Vents Bacterial; isolated from a
 PCR-generated bacterial clone library, Appl. Environ.
 Microbiol. 60:871-879"